

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/824,178

DATE: 04/26/2001
TIME: 22:18:59

INPUT SET: S36619.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#2

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Jean-Marc Roch
6 Victoria E.S. Scott
7 Kristi L. Anderson
8 James P. Sullivan
9
10 (ii) TITLE OF INVENTION: HUMAN ENDOSULFINE GENE
11
12 (iii) NUMBER OF SEQUENCES: 13
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Abbott Laboratories
16 (B) STREET: 100 Abbott Park Road
17 (C) CITY: Abbott Park
18 (D) STATE: Illinois
19 (E) COUNTRY: USA
20 (F) ZIP: 60064-3500
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: Macintosh
25 (C) OPERATING SYSTEM: System 7.0.1
26 (D) SOFTWARE: MS Word
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: 09/824,178
30 (B) FILING DATE:
31 (C) CLASSIFICATION:
32
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 08/779,775
36 (B) FILING DATE:
37
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Priscilla E. Porembski
41 (B) REGISTRATION NUMBER: 33,207
42 (C) DOCKET NUMBER: 6024.US.01
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 708/937-0378
46 (B) TELEFAX: 708/938-2623

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47 (C) TELEX:

48

49

50 (2) INFORMATION FOR SEQ ID NO:1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 1103 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: double

55 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: cDNA

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

58

59	GTGACAGGAG	CCGAAGCAGC	AGCGCAGGTT	GTCCCCGTTT	CCCCTCCCCC	TTCCCTTCTC	60
60	CGGTTGCCTT	CCCGGGCCCC	TTACTACTCCA	CAGTCCCAGT	CCCGCCATGT	CCCAGAAACA	120
61	AGAAGAAGAG	AACCCTGCGG	AGGAGACCGG	CGAGGAGAAG	CAGGACACGC	AGGAGAAAGA	180
62	AGGTATTCTG	CCTGAGAGAG	CTGAAGAGGC	AAAGCTAAAG	GCCAAATACC	CAAGCCTAGG	240
63	ACAAAAGCCT	GGAGGCTCCG	ACTTCCTCAT	GAAGAGACTC	CAGAAAGGGC	AAAAGTACTT	300
64	TGACTCAGGA	GACTACAACA	TGGCCAAAGC	CAAGATGAAG	AATAAGCAGC	TGCCAAGTGC	360
65	AGGACCAGAC	AAGAACCTGG	TGACTGGTGA	TCACATCCCC	ACCCACACAG	ATCTGCCCCA	420
66	GAGAAAGTCC	TCGCTCGTCA	CCAGCAAGCT	TGCGGGGTAA	CCTGAGCCCC	CCTCTCCTCC	480
67	CCTTCTCAA	CCACTGGACG	TTTATATATT	ATAGGCAGGG	ATGAAATGGG	CACCTAGTCA	540
68	GATCTTCTCA	GCTTGCTAGC	CAGAAATGAC	TGTGATTCTG	CTGGGGGCTG	CTGAGAAGGT	600
69	AATGTAGGTT	GAAAAGGGGC	TCTAAGTTTA	TTTATTTCTG	TAGATTGACA	CTTCCACACA	660
70	CTCCCTGTAG	TCCAGGTAGG	GCCTAGAAAT	AGGAAAGGCT	AGGATTGGAT	AATGCTGCAA	720
71	ATGCTTTTTT	TGTGTGAGAA	ACTGGAGAGA	TGTGATTCTT	CCTTTTGGA	GAGAATGTCC	780
72	CAAATTTGAT	TAGGCTGAGC	CTTGGGAATA	GTTTGGCAGG	TTTAACATCC	CAAGGCTAAC	840
73	CTAACGTAAG	TGGGAAAGGT	AGATTGAATG	AGACATGTTT	TCTGTGCTTC	TAAGTGTTCT	900
74	GTCCCTTAGG	CTGCTATTGC	TTTATGTTTC	CATTATGGCA	GGTTTAGAGA	ATCCTTAAAA	960
75	AGAAAAATTG	ACTTGCTTGC	CTAAACTAC	AGTGCCCCCT	TAGCCTCCAT	TACTTAGTAT	1020
76	CTCTTACAGT	TTGCTCTGGC	TCTCAAATAA	TATAAAGATT	GATGAACATT	ATTCACAAAA	1080
77	AAAAAAAAAA	AAAGGGCGGC	GCG				1103

78

79

80 (2) INFORMATION FOR SEQ ID NO:2:

81 (i) SEQUENCE CHARACTERISTICS:

82 (A) LENGTH: 1199 base pairs

83 (B) TYPE: nucleic acid

84 (C) STRANDEDNESS: double

85 (D) TOPOLOGY: linear

86 (ii) MOLECULE TYPE: cDNA

87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

88

89	GTGACAGGAG	CCGAAGCAGC	AGCGCAGGTT	GTCCCCGTTT	CCCCTCCCCC	TTCCCTTCTC	60
90	CGGTTGCCTT	CCCGGGCCCC	TTACTACTCCA	CAGTCCCAGT	CCCGCCATGT	CCCAGAAACA	120
91	AGAAGAAGAG	AACCCTGCGG	AGGAGACCGG	CGAGGAGAAG	CAGGACACGC	AGGAGAAAGA	180
92	AGGTATTCTG	CCTGAGAGAG	CTGAAGAGGC	AAAGCTAAAG	GCCAAATACC	CAAGCCTAGG	240
93	ACAAAAGCCT	GGAGGCTCCG	ACTTCCTCAT	GAAGAGACTC	CAGAAAGGGC	AAAAGTACTT	300
94	TGACTCAGGA	GACTACAACA	TGGCCAAAGC	CAAGATGAAG	AATAAGCAGC	TGCCAAGTGC	360
95	AGGACCAGAC	AAGAACCTGG	TGACTGGTGA	TCACATCCCC	ACCCACACAG	ATCTGCCCCA	420
96	GAGAAAGTCC	TCGCTCGTCA	CCAGCAAGCT	TGCGGGTGGC	CAAGTTGAAT	GATGCTGCCC	480
97	GGGGCTCTGC	CAGATCCTGA	GACTGCTTTT	GCCGCTTCCC	CTCCCTGCCC	CACCCGGGTC	540
98	CTGTGCTGGC	TCCTGCCCTT	TCAGCCAGGG	GTCAGGAGGT	GGCTCGGGTG	TGGGCTGGAG	600
99	AGGCAGAAGC	CCTTTCCTGT	TGGTGTCCTA	GCACATGGAG	CCCCTTGGGC	TGAGCACCAA	660

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100 GACCTTGAAC CTTTTTGTG TTACCTTTTT TCCAAATAAC AGTTGGGAGA AATATCAATG 720
101 AAATTCTGGG GGTGGGGGTG GGGCTGAAAG GGTGGGGTGG GAGATATGGA GGAGTATGAA 780
102 TTAGGGCTTG GAGTTGCTAA AACATTTCCT GACTATCCTT CTTAACCACG TGGCTGATGT 840
103 GGGGTAGGTA TGAGGGGAAG GAAGTGGAGT AGCCTAATGA AAAGGGGTTC TAGTTGAGCT 900
104 CTGTAGATAA ATGCCTTGTG TCAGTGTGGT TGGAGACCTG GTGTCAGATA AAAGAAACTC 960
105 CATCCGCACA GACAGATGCA AACAGCTCCT CTAGTTCTGC AGAGCTAGTT GAGAACTCAA 1020
106 CATTAATCAT TTTAAAAAGT ACTGTCCTTG AAATAGATTG GCTGTGGGAA GAAGGGCAGT 1080
107 GAGTGTGGGA GAAAGGAGCC GTGAGCGTGG GGAACCCAC AGAGCCCAA GGACTTTTTC 1140
108 AGTATTCGAA ATAAACAAAA CAAAAACCCA TGAAAAAACC CAAAAAATAA AAAAAAATAA 1199

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109
110

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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119
120 Met Ser Gln Lys Gln Glu Glu Asn Pro Ala Glu Glu Thr Gly Glu
121 1 5 10 15
122 Glu Lys Gln Asp Thr Gln Glu Lys Glu Gly Ile Leu Pro Glu Arg Ala
123 20 25 30
124 Glu Glu Ala Lys Leu Lys Ala Lys Tyr Pro Ser Leu Gly Gln Lys Pro
125 35 40 45
126 Gly Gly Ser Asp Phe Leu Met Lys Arg Leu Gln Lys Gly Gln Lys Tyr
127 50 55 60
128 Phe Asp Ser Gly Asp Tyr Asn Met Ala Lys Ala Lys Met Lys Asn Lys
129 65 70 75 80
130 Gln Leu Pro Ser Ala Gly Pro Asp Lys Asn Leu Val Thr Gly Asp His
131 85 90 95
132 Ile Pro Thr Pro Gln Asp Leu Pro Gln Arg Lys Ser Ser Leu Val Thr
133 100 105 110
134 Ser Lys Leu Ala Gly

```

135 115

136
137

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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146
147 Met Ser Gln Lys Gln Glu Glu Asn Pro Ala Glu Glu Thr Gly Glu
148 1 5 10 15
149 Glu Lys Gln Asp Thr Gln Glu Lys Glu Gly Ile Leu Pro Glu Arg Ala
150 20 25 30
151 Glu Glu Ala Lys Leu Lys Ala Lys Tyr Pro Ser Leu Gly Gln Lys Pro
152 35 40 45

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153 Gly Gly Ser Asp Phe Leu Met Lys Arg Leu Gln Lys Gly Gln Lys Tyr
154 50 55 60
155 Phe Asp Ser Gly Asp Tyr Asn Met Ala Lys Ala Lys Met Lys Asn Lys
156 65 70 75 80
157 Gln Leu Pro Ser Ala Gly Pro Asp Lys Asn Leu Val Thr Gly Asp His
158 85 90 95
159 Ile Pro Thr Pro Gln Asp Leu Pro Gln Arg Lys Ser Ser Leu Val Thr
160 100 105 110
161 Ser Lys Leu Ala Gly Gly Gln Val Glu
162 115 120
163
164

- 165 (2) INFORMATION FOR SEQ ID NO:5:
166 (i) SEQUENCE CHARACTERISTICS:
167 (A) LENGTH: 20 base pairs
168 (B) TYPE: nucleic acid
169 (C) STRANDEDNESS: single
170 (D) TOPOLOGY: linear
171 (ii) MOLECULE TYPE: DNA
172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
173

174 GAAGAGACTC CAGAAAGGGC 20
175
176

- 177 (2) INFORMATION FOR SEQ ID NO:6:
178 (i) SEQUENCE CHARACTERISTICS:
179 (A) LENGTH: 20 base pairs
180 (B) TYPE: nucleic acid
181 (C) STRANDEDNESS: single
182 (D) TOPOLOGY: linear
183 (ii) MOLECULE TYPE: DNA
184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
185

186 GAAGCAATAG CAGCCTAAGG 20
187

- 188
189 (2) INFORMATION FOR SEQ ID NO:7:
190 (i) SEQUENCE CHARACTERISTICS:
191 (A) LENGTH: 19 base pairs
192 (B) TYPE: nucleic acid
193 (C) STRANDEDNESS: single
194 (D) TOPOLOGY: linear
195 (ii) MOLECULE TYPE: DNA
196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
197

198 TGTGCTGGGA CACCAACAG 19
199
200

- 201 (2) INFORMATION FOR SEQ ID NO:8:
202 (i) SEQUENCE CHARACTERISTICS:
203 (A) LENGTH: 29 base pairs
204 (B) TYPE: nucleic acid
205 (C) STRANDEDNESS: single

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206 (D) TOPOLOGY: linear
207 (ii) MOLECULE TYPE: DNA
208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
209
210 GGAAGGCGCC ATGTCCCAGA AACAAGAAG 29
211
212
213 (2) INFORMATION FOR SEQ ID NO:9:
214 (i) SEQUENCE CHARACTERISTICS:
215 (A) LENGTH: 29 base pairs
216 (B) TYPE: nucleic acid
217 (C) STRANDEDNESS: single
218 (D) TOPOLOGY: linear
219 (ii) MOLECULE TYPE: DNA
220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
221
222 CAAAGTCGAC TTACCCCGCA AGCTTGCTG 29
223
224
225 (2) INFORMATION FOR SEQ ID NO:10:
226 (i) SEQUENCE CHARACTERISTICS:
227 (A) LENGTH: 29 base pairs
228 (B) TYPE: nucleic acid
229 (C) STRANDEDNESS: single
230 (D) TOPOLOGY: linear
231 (ii) MOLECULE TYPE: DNA
232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
233
234 CCAAGTCGAC TCATTCAACT TGGCCACCC 29
235
236
237 (2) INFORMATION FOR SEQ ID NO:11:
238 (i) SEQUENCE CHARACTERISTICS:
239 (A) LENGTH: 111 amino acids
240 (B) TYPE: amino acid
241 (C) STRANDEDNESS: single
242 (D) TOPOLOGY: linear
243 (ii) MOLECULE TYPE: protein
244 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
245
246 Met Ser Ala Glu Val Pro Glu Ala Ala Ser Ala Glu Glu Gln Lys Glu
247 1 5 10 15
248 Met Glu Asp Lys Val Thr Pro Glu Lys Ala Glu Glu Ala Lys Leu Lys
249 20 25 30
250 Ala Arg Tyr Pro His Leu Gly Gln Lys Pro Gly Gly Ser Asp Phe Leu
251 35 40 45
252 Arg Lys Arg Leu Gln Lys Gly Gln Lys Tyr Phe Asp Ser Gly Asp Tyr
253 50 55 60
254 Asn Met Ala Lys Ala Lys Met Lys Asn Lys Gln Leu Pro Thr Ala Thr
255 65 70 75 80
256 Pro Asp Lys Thr Glu Val Thr Gly Asp His Ile Pro Thr Pro Gln Asp
257 85 90 95
258 Leu Pro Gln Arg Lys Pro Ser Leu Val Arg Ser Lys Leu Ala Gly

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/824,178

DATE: 04/26/2001
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Line

Error

Original Text

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/824,178

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INPUT SET: S36619.raw

< < THERE ARE NO ITEMS MISSING > >

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/824,178

DATE: 04/26/2001
TIME: 22:19:01

INPUT SET: S36619.raw

Line	Original Text	Corrected Text
42	(C) DOCKET NUMBER: 6024.US.O1	(C) REFERENCE/DOCKET NUMBER: 6024.US.O1